IN THE CLAIMS

Please substitute the pending set of claims with this set of claims.

1. (Original) A composition comprising a plurality of beads, wherein each of said plurality of beads comprises a plurality of bound polynucleotides, wherein the polynucleotides in the composition are heterogeneous, and wherein on at least 1 % of said beads the plurality of bound polynucleotides is homogeneous.
2. (Original) The composition of claim 1 wherein on at least 5 % of said beads the plurality of bound polynucleotides is homogeneous.
3. (Original) The composition of claim 1 wherein on at least 10 % of said beads the plurality of bound polynucleotides is homogeneous.
4. (Original) The composition of claim 1 wherein on at least 50 % of said beads the plurality of bound polynucleotides is homogeneous.
5. (Original) The composition of claim 1 wherein the plurality of bound polynucleotides is greater than 100.
6. (Original) The composition of claim 1 which is a liquid.
7. (Original) The composition of claim 6 which comprises agarose.
8. (Original) The composition of claim 1 wherein the polynucleotides in the composition differ by a single nucleotide polymorphism (SNP).
9. (Original) The composition of claim 1 wherein the polynucleotides in the composition differ in the presence or absence of a mutation.
10. (Original) The composition of claim 1 wherein the polynucleotides in the composition differ in the presence or absence of an insertion.
11. (Original) The composition of claim 1 wherein the polynucleotides in the composition differ by the presence or absence of a polymorphism.
12. (Original) The composition of claim 1 wherein the beads are magnetic.
13. (Original) The composition of claim 1 wherein at least one species of polynucleotide is labeled with a fluorescent dye.

14. (Original) The composition of claim 13 wherein the labeling is via a labeled oligonucleotide.

15. (Original) The composition of claim 13 wherein the labeling is via one or more labeled antibodies.

16. (Original) The composition of claim 1 wherein the bound polynucleotides were made by amplification of a template in a test sample, wherein the beads on which the plurality of bound polynucleotides is homogeneous comprise at least a first and a second species of polynucleotide, wherein the beads comprising the first species of polynucleotide and the beads comprising the second species of polynucleotide are present in the composition in the same ratio as the first and second species of polynucleotide were present in the test sample.

17. (Original) A liquid composition comprising a plurality of microemulsions forming aqueous compartments wherein at least a portion of said aqueous compartments comprise:

a bead;

a polynucleotide template; and

oligonucleotide primers for amplifying said template;

wherein at least a portion of the oligonucleotide primers is bound to the bead.

18. (Original) The liquid composition of claim 17 which comprises forward and reverse oligonucleotide primers.

19. (Original) The liquid composition of claim 17 wherein said aqueous compartments have an average diameter of 0.5 to 50 microns.

20. (Original) The liquid composition of claim 17 wherein at least one in 10,000 of said aqueous compartments comprise a bead.

21. (Original) The liquid composition of claim 17 wherein from 1/100 to 1 of said aqueous compartments comprise a bead.

22. (Original) The liquid composition of claim 17 wherein from 1/50 to 1 of said aqueous compartments comprise a polynucleotide template molecule.

23. (Original) The liquid composition of claim 17 wherein the bead is magnetic.

24. (Original) The liquid composition of claim 17 wherein the average number of template molecules per aqueous compartment is less than 1.

25. (Original) The liquid composition of claim 17 further comprising a DNA polymerase and deoxyribonucleotides.

26. (Original) The liquid composition of claim 17 wherein the average diameter of said aqueous compartments is from 1 to 10 microns, inclusive.

27. (Original) The liquid composition of claim 17 wherein the average diameter of said aqueous compartments is from 11 to 100 microns, inclusive.

28. (Original) The liquid composition of claim 17 wherein the average diameter of said aqueous compartments is about 5 microns.

29. (Original) The liquid composition of claim 17 wherein each oligonucleotide primer is at least 12 nucleotides in length.

30. (Original) The liquid composition of claim 17 wherein each oligonucleotide primer is from 25 to 55 nucleotides.

31. (Original) The liquid composition of claim 17 wherein binding of said oligonucleotide primers to said bead is covalent.

32. (Original) The liquid composition of claim 17 wherein binding of said oligonucleotide primers to said bead is via a biotin-streptavidin binding pair.

33. (Original) The liquid composition of claim 32 wherein said forward or reverse oligonucleotide primers that are bound to said bead comprise at least two biotin moieties.

34. (Original) The liquid composition of claim 17 wherein the aqueous compartments comprise agarose.

35. (Original) A method for analyzing nucleotide sequence variations, comprising:

forming microemulsions comprising one or more species of analyte DNA molecules;

amplifying analyte DNA molecules in the microemulsions in the presence of reagent beads, wherein the reagent beads are bound to a plurality of molecules of a primer for amplifying the analyte DNA molecules, whereby product beads are formed which are bound to a plurality of copies of one species of analyte DNA molecule;

separating the product beads from analyte DNA molecules which are not bound to

product beads;

determining a sequence feature of the one species of analyte DNA molecule which is bound to the product beads.

36. (Original) The method of claim 35 further comprising the step of isolating product beads which are bound to a plurality of copies of a first species of analyte DNA molecule from product beads which are bound to a plurality of copies of a second species of analyte DNA molecule.

37. (Original) The method of claim 36 wherein the step of isolating is performed using fluorescence activated cell sorting.

38. (Original) The method of claim 36 further comprising the step of recovering the first species of analyte DNA molecule from the product beads.

39. (Original) The method of claim 36 further comprising the step of amplifying the first species of analyte DNA molecule from the isolated product beads.

40. (Original) The method of claim 38 further comprising the step of determining the sequence of the first species of analyte DNA molecule.

41. (Original) The method of claim 35 wherein the step of amplifying converts less than 10 % of the reagent beads present in the microemulsions into product beads.

42. (Original) The method of claim 35 wherein prior to the step of separating, the microemulsions are broken by addition of one or more detergents.

43. (Original) The method of claim 35 wherein the step of determining is performed by hybridization to oligonucleotide probes which are differentially labeled.

44. (Original) The method of claim 35 wherein the relative or absolute amounts of product beads comprising one or more sequence features is determined.

45. (Original) The method of claim 44 wherein the relative or absolute amounts are determined using flow cytometery.

46. (Original) The method of claim 35 wherein the step of amplifying employs additional copies of the primer which are not bound to the reagent bead.

47. (Original) The method of claim 35 wherein the analyte DNA molecules are genomic DNA.

48. (Original) The method of claim 35 wherein the analyte DNA molecules are cDNA.

49. (Original) The method of claim 35 wherein the analyte DNA molecules are PCR products made from genomic DNA.

50. (Original) The method of claim 35 wherein the analyte DNA molecules are PCR products made from cDNA.

51. (Original) The method of claim 35 wherein the analyte DNA molecules are derived from a single individual.

52. (Original) The method of claim 35 wherein the analyte DNA molecules are derived from a population of individuals.

53. (Original) The method of claim 35 wherein the reagent beads are magnetic.

54. (Original) The method of claim 35 wherein the step of determining a sequence feature is performed by extension of a primer with one or more labeled deoxyribonucleotides.

55. (Original) A probe for use in hybridization to a polynucleotide that is bound to a solid support, comprising:

an oligonucleotide with a stem-loop structure having a photoluminescent dye at one of the 5' or 3' ends, wherein said oligonucleotide does not comprise a quenching agent at the opposite 5' or 3' end.

56. (Original) The probe of claim 55 which hybridizes to a wild-type selected genetic sequence better than to a mutant selected genetic sequence.

57. (Original) The probe of claim 55 which hybridizes to a mutant genetic sequence better than to a wild-type genetic sequence.

58. (Original) A pair of molecular probes comprising:

a first oligonucleotide with a stem-loop structure having a first photoluminescent dye at one of the 5' or 3' ends, wherein said first oligonucleotide does not comprise a quenching agent at the opposite 5' or 3' end, wherein said first oligonucleotide hybridizes to a wild-type selected genetic sequence better than to a mutant selected genetic sequence; and

a second oligonucleotide with a stem-loop structure having a second photoluminescent dye at one of the 5' or 3' ends, wherein said second oligonucleotide does not comprise a quenching agent at the opposite 5' or 3' end, wherein said second oligonucleotide hybridizes to the mutant selected genetic sequence better than to the

wild-type selected genetic sequence;

wherein the first and the second photoluminescent dyes are distinct.

59. (Original) A method for isolating nucleotide sequence variants, comprising:

forming microemulsions comprising one or more species of analyte DNA molecules;

amplifying analyte DNA molecules in the microemulsions in the presence of reagent beads, wherein the reagent beads are bound to a plurality of molecules of a primer for amplifying the analyte DNA molecules, whereby product beads are formed which are bound to a plurality of copies of one species of analyte DNA molecule;

separating the product beads from analyte DNA molecules which are not bound to product beads;

isolating product beads which are bound to a plurality of copies of a first species of analyte DNA molecule from product beads which are bound to a plurality of copies of a second species of analyte DNA molecule.

60. (Original) The method of claim 59 wherein the step of isolating is performed using fluorescence activated cell sorting.

61. (Original) The method of claim 59 further comprising the step of recovering the first species of analyte DNA molecule from the product beads.

62. (Original) The method of claim 59 further comprising the step of amplifying the first species of analyte DNA molecule from the isolated product beads.

63. (Original) The method of claim 59 further comprising the step of determining the sequence of the first species of analyte DNA molecule.

64. (New) A method for amplifying a nucleic acid molecule comprising the steps of: (a) forming aqueous compartments in a water-in-oil emulsion, wherein a plurality of compartments include a nucleic acid molecule, a bead capable of being linked to the nucleic acid molecule, and an aqueous solution comprising components necessary to perform nucleic acid amplification; (b) amplifying the nucleic acid molecule in the compartments to form amplified product copies of the nucleic acid molecule; and (c) capturing the amplified product copies to the bead in the compartments, thereby amplifying of the nucleic acid molecule.

65. (New) The method of claim 64, wherein the nucleic acid amplification is performed using polymerase chain reaction.

66. (New) The method of claim 64 wherein the emulsion comprises a detergent.

67. (New) The method of claim 64 wherein the nucleic acid amplification is performed using polymerase chain reaction, and the emulsion is thermostable.

68. (New) The method of claim 64 wherein the nucleic acid molecule is genomic DNA or cDNA.

69. (New) The method of claim 64 wherein a plurality of compartments when formed each contains on average less than one nucleic acid molecule.

70. (New) A method for amplifying a nucleic acid molecule comprising the steps of: (a) forming aqueous compartments in a water-in-oil emulsion, wherein a plurality of the compartments include a nucleic acid molecule, and an aqueous solution comprising components necessary for nucleic acid amplification; (b) amplifying the nucleic acid molecule in the compartments to form amplified copies of the nucleic acid molecule.

71. (New) The method of claim 70 wherein the nucleic acid amplification is performed using polymerase chain reaction.

72. (New) The method of claim 70 wherein the emulsion is thermostable.

73. (New) The method of claim 70 wherein the amplified copies of the nucleic acid molecule are linked to a bead.

74. (New) The method of claim 73 wherein the nucleic acid amplification is performed using polymerase chain reaction, and the emulsion is thermostable.

75. (New) The method of claim 70 wherein a plurality of compartments when formed each contains on average less than one nucleic acid molecule.

76. (New) A method for amplifying one or more nucleic acids comprising the steps of: (a) forming a water-in-oil emulsion to create a plurality of aqueous compartments wherein at least one of the compartments comprises a single nucleic acid template, a single bead capable of binding to the nucleic acid, and amplification reaction solution containing reagents necessary to perform nucleic acid amplification; (b) amplifying the nucleic acids in the compartments to form amplified copies of said nucleic acids; and (c) binding the amplified copies to the beads in the compartments.

77. (New) The method of claim 76 wherein said emulsion is heat stable.

78. (New) The method of claim 76, wherein the bead comprises a member of a binding pair and the binding pair is avidin/biotin.

79. (New) A method for sequencing nucleic acids comprising: (a) fragmenting large template nucleic acid molecules to generate a plurality of fragmented nucleic acids; (b) delivering the fragmented nucleic acids into aqueous compartments in a water-in-oil emulsion such that a plurality of aqueous compartments comprise a single copy of a fragmented nucleic acid, a single bead capable of binding to the fragmented nucleic acid, and amplification reaction solution containing reagents necessary to perform nucleic acid amplification; (c) amplifying the fragmented nucleic acids in the compartments to form amplified copies of said nucleic acids and binding the amplified copies to beads in the compartments; (d) delivering the beads to an array, and (e) performing a sequencing reaction simultaneously on a plurality of the reaction chambers.

80. (New) A method for delivering a nucleic acid template to an array, comprising dispersing over the array a plurality of beads, each bead having at least one nucleic acid template immobilized thereon, wherein the nucleic acid template is suitable for use in a nucleic acid sequencing reaction.

81. (New) A method for sequencing nucleic acids comprising: (a) fragmenting nucleic acid molecules to generate a plurality of fragmented nucleic acids; (b) attaching one strand of a plurality of the fragmented nucleic acids individually to beads to generate single stranded nucleic acids attached individually to beads; (c) delivering a population of the single stranded fragmented nucleic acids attached individually to beads to an array; (d) performing a sequencing reaction simultaneously on a plurality of the reaction chambers.

82. (New) A method for delivering nucleic acid templates to an array comprising the steps of: (a) providing a population of nucleic acid templates; (b) isolating each nucleic acid template from said population to a bead; (c) delivering a population of said nucleic acid templates isolated to a bead to said array.

83. (New) The method of claim 82, wherein said isolating step comprises encapsulating said nucleic acid template in an emulsion of a water-in-oil emulsion.

84. (New) The method of claim 82, wherein said nucleic acid template is encapsulated with a bead and wherein the bead can bind said nucleic acid.